

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101532,153

Source: PCT

Date Processed by STIC: 4-28-05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 04/28/2005

PATENT APPLICATION: US/10/532,153

TIME: 16:26:58

Input Set : A:\Seq Listing.ST25.txt

Output Set: N:\CRF4\04272005\J532153.raw

3 <110> APPLICANT: Evolutionary Genomics LLC
 5 <120> TITLE OF INVENTION: Development of Therapeutics for the Treatment of
 6 Endotoxin-Mediated Diseases
 8 <130> FILE REFERENCE: GENO200.3.1
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/532,153
 C--> 10 <141> CURRENT FILING DATE: 2005-04-20
 10 <150> PRIOR APPLICATION NUMBER: 10/100,422
 11 <151> PRIOR FILING DATE: 2002-03-18
 13 <160> NUMBER OF SEQ ID NOS: 40
 15 <170> SOFTWARE: PatentIn version 3.2
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2427
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Pan troglodytes
 22 <400> SEQUENCE: 1
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 27 tatagcttct tcagtttccc agaactgcag gtgctggatt tatccagggtg tgaaatccag 180
 29 acaattgaag atggggcata tcagagccta agccacctct ccaccttaat attgacagga 240
 31 aaccccatcc agagtttagc cctgggagcc ttttctggac tatcaagttt acagaagctg 300
 33 gtggctgtgg agacaaatct agcatctcta gagaacttcc ccattggaca tctcaaaact 360
 35 ttgaaagaac ttaatgtggc tcacaatctt atccaatctt tcaaattacc tgagtatttt 420
 37 tctaactctga ccaatctaga gcacttggac ctttccagca acaagattca aagtatttat 480
 39 tgcacagact tgcgggttct acatcaaagc cccctactca atctctcttt agacctgtcc 540
 41 ctgaacccta tgaactttat ccaaccagggt gcatttaaag aaattagggt tcataagctg 600
 43 actttgagaa ataattttga tagtttaaat gtaatgaaaa cttgtattca aggtctggct 660
 45 ggttttagaag tccatcgttt ggttctggga gaatttagaa atgaaggaaa cttggaaaag 720
 47 tttgacaaat ctgctctaga gggcctgtgc aatttgacca ttgaagaatt ccgattagca 780
 49 tacttagact actacctcga tgatattatt gacttattta attgtttgac aaatgtttct 840
 51 tcattttccc tgggtgagtgt gactattaaa agcgtaaaag acttttctta taatttcgga 900
 53 tggcaacatt tagaattagt taactgtaaa tttggacagt tcccacatt gaaactcaaa 960
 55 tctctcaaaa ggcttacttt cacttccaac aaaggtggga atgctttttc agaagttgat 1020
 57 ctaccaagcc ttgagtttct agatctcagt agaaatggct tgagtttcaa aggttgctgt 1080
 59 tctcaaagtg attttgggac aaccagccta aagtatttag atctgagctt caatggtgtt 1140
 61 attaccatga gttcaaactt cttgggctta gaacaactag aacatctgga tttccagcat 1200
 63 tccaatttga aacaaatgag tgagttttca gtattcctat cactcagaaa cctcatttac 1260
 65 cttgacattt ctcatactca caccagagtt gctttcaatg gcatcttcaa tggcttgtcc 1320
 67 agtctcgaag tcttgaaaaat ggctggcaat tctttccagg aaaacttctt tccagatatc 1380
 69 ttcacagagc tgagaaactt gaccttccgt gacctctctc agtgtcaact ggagcagttg 1440
 71 tctccaacag catttaactc actctccagt cttcaggtac taaatatgag ccacaacaac 1500
 73 ttcttttcat tggatacgtt tctttataag tgtctgaact ccctccagggt tcttgattac 1560
 75 agtctcaatc acataatgac ttccaaaaaa caggaactac agcattttcc aagtagtcta 1620
 77 gctttcttaa atcttactca gaatgacttt gcttgacttt gtgaacacca aagtttctctg 1680

(pg. 6)

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81 ccttcagata agcagggcat gcctgtgctg agtttgaata tcacctgtca gatgaataag 1800
83 accatcattg gtgtgtcggt cctcagtgctg cttgtagtat ctgttgtagc agttctggtc 1860
85 tataagttct attttcacct gatgcttctt gctggctgca taaagtatgg tagaggtgaa 1920
87 aacatctatg atgcctttgt tatctactca agccaggatg aggactgggt aaggaatgag 1980
89 ctagtaaaga atttagaaga aggggtgcct ccatttcagc tctgccttca ctacagagac 2040
91 tttattcccg gtgtggccat tgctgccaac atcatccatg aaggtttcca taaaagccga 2100
93 aaggtgattg ttgtggtgtc ccagcacttc atccagagcc gctggtgtat ctttgaatat 2160
95 gagattgctc agacctggca gtttctgagc agtcgtgctg gtatcatctt cattgtcctg 2220
97 cagaaggtgg agaagaccct gctcaggcgg caggtggagc tgtaccgcct tctcagcagg 2280
99 aacacttacc tggagtggga ggacagtgtc ctggggcggc acatcttctg gagacgactc 2340
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107 <211> LENGTH: 2427
108 <212> TYPE: DNA
109 <213> ORGANISM: Pan troglodytes
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113 <221> NAME/KEY: CDS
114 <222> LOCATION: (1)..(2427)
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119 1 5 10 15
121 atc ccc gac aac ctc ccc ttc tca acc aag aac ctg gac ctg agc ttt 96
122 Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe
123 20 25 30
125 aat ccc ctg agg cat tta ggc agc tat agc ttc ttc agt ttc cca gaa 144
126 Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu
127 35 40 45
129 ctg cag gtg ctg gat tta tcc agg tgt gaa atc cag aca att gaa gat 192
130 Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp
131 50 55 60
133 ggg gca tat cag agc cta agc cac ctc tcc acc tta ata ttg aca gga 240
134 Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly
135 65 70 75 80
137 aac ccc atc cag agt tta gcc ctg gga gcc ttt tct gga cta tca agt 288
138 Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser
139 85 90 95
141 tta cag aag ctg gtg gct gtg gag aca aat cta gca tct cta gag aac 336
142 Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn
143 100 105 110
145 ttc ccc att gga cat ctc aaa act ttg aaa gaa ctt aat gtg gct cac 384
146 Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His
147 115 120 125
149 aat ctt atc caa tct ttc aaa tta cct gag tat ttt tct aat ctg acc 432
150 Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr
151 130 135 140
153 aat cta gag cac ttg gac ctt tcc agc aac aag att caa agt att tat 480

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155	145					150					155					160	
157	tgc	aca	gac	ttg	cgg	gtt	cta	cat	caa	atg	ccc	cta	ctc	aat	ctc	tct	528
158	Cys	Thr	Asp	Leu	Arg	Val	Leu	His	Gln	Met	Pro	Leu	Leu	Asn	Leu	Ser	
159					165					170					175		
161	tta	gac	ctg	tcc	ctg	aac	cct	atg	aac	ttt	atc	caa	cca	ggt	gca	ttt	576
162	Leu	Asp	Leu	Ser	Leu	Asn	Pro	Met	Asn	Phe	Ile	Gln	Pro	Gly	Ala	Phe	
163				180						185					190		
165	aaa	gaa	att	agg	ctt	cat	aag	ctg	act	ttg	aga	aat	aat	ttt	gat	agt	624
166	Lys	Glu	Ile	Arg	Leu	His	Lys	Leu	Thr	Leu	Arg	Asn	Asn	Phe	Asp	Ser	
167			195					200					205				
169	tta	aat	gta	atg	aaa	act	tgt	att	caa	ggt	ctg	gct	ggt	tta	gaa	gtc	672
170	Leu	Asn	Val	Met	Lys	Thr	Cys	Ile	Gln	Gly	Leu	Ala	Gly	Leu	Glu	Val	
171		210					215					220					
173	cat	cgt	ttg	gtt	ctg	gga	gaa	ttt	aga	aat	gaa	gga	aac	ttg	gaa	aag	720
174	His	Arg	Leu	Val	Leu	Gly	Glu	Phe	Arg	Asn	Glu	Gly	Asn	Leu	Glu	Lys	
175	225				230					235					240		
177	ttt	gac	aaa	tct	gct	cta	gag	ggc	ctg	tgc	aat	ttg	acc	att	gaa	gaa	768
178	Phe	Asp	Lys	Ser	Ala	Leu	Glu	Gly	Leu	Cys	Asn	Leu	Thr	Ile	Glu	Glu	
179				245						250					255		
181	ttc	cga	tta	gca	tac	tta	gac	tac	tac	ctc	gat	gat	att	att	gac	tta	816
182	Phe	Arg	Leu	Ala	Tyr	Leu	Asp	Tyr	Tyr	Leu	Asp	Asp	Ile	Ile	Asp	Leu	
183			260						265					270			
185	ttt	aat	tgt	ttg	aca	aat	gtt	tct	tca	ttt	tcc	ctg	gtg	agt	gtg	act	864
186	Phe	Asn	Cys	Leu	Thr	Asn	Val	Ser	Ser	Phe	Ser	Leu	Val	Ser	Val	Thr	
187		275						280					285				
189	att	aaa	agc	gta	aaa	gac	ttt	tct	tat	aat	ttc	gga	tgg	caa	cat	tta	912
190	Ile	Lys	Ser	Val	Lys	Asp	Phe	Ser	Tyr	Asn	Phe	Gly	Trp	Gln	His	Leu	
191		290				295					300						
193	gaa	tta	gtt	aac	tgt	aaa	ttt	gga	cag	ttt	ccc	aca	ttg	aaa	ctc	aaa	960
194	Glu	Leu	Val	Asn	Cys	Lys	Phe	Gly	Gln	Phe	Pro	Thr	Leu	Lys	Leu	Lys	
195	305				310					315					320		
197	tct	ctc	aaa	agg	ctt	act	ttc	act	tcc	aac	aaa	ggt	ggg	aat	gct	ttt	1008
198	Ser	Leu	Lys	Arg	Leu	Thr	Phe	Thr	Ser	Asn	Lys	Gly	Gly	Asn	Ala	Phe	
199				325						330					335		
201	tca	gaa	gtt	gat	cta	cca	agc	ctt	gag	ttt	cta	gat	ctc	agt	aga	aat	1056
202	Ser	Glu	Val	Asp	Leu	Pro	Ser	Leu	Glu	Phe	Leu	Asp	Leu	Ser	Arg	Asn	
203			340						345					350			
205	ggc	ttg	agt	ttc	aaa	ggt	tgc	tgt	tct	caa	agt	gat	ttt	ggg	aca	acc	1104
206	Gly	Leu	Ser	Phe	Lys	Gly	Cys	Cys	Ser	Gln	Ser	Asp	Phe	Gly	Thr	Thr	
207		355					360						365				
209	agc	cta	aag	tat	tta	gat	ctg	agc	ttc	aat	ggt	gtt	att	acc	atg	agt	1152
210	Ser	Leu	Lys	Tyr	Leu	Asp	Leu	Ser	Phe	Asn	Gly	Val	Ile	Thr	Met	Ser	
211		370				375						380					
213	tca	aac	ttc	ttg	ggc	tta	gaa	caa	cta	gaa	cat	ctg	gat	ttc	cag	cat	1200
214	Ser	Asn	Phe	Leu	Gly	Leu	Glu	Gln	Leu	Glu	His	Leu	Asp	Phe	Gln	His	
215	385				390					395					400		
217	tcc	aat	ttg	aaa	caa	atg	agt	gag	ttt	tca	gta	ttc	cta	tca	ctc	aga	1248
218	Ser	Asn	Leu	Lys	Gln	Met	Ser	Glu	Phe	Ser	Val	Phe	Leu	Ser	Leu	Arg	

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219		405		410		415		
221	aac ctc att tac ctt gac att tct cat act cac acc aga gtt gct ttc							1296
222	Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe							
223		420		425		430		
225	aat ggc atc ttc aat ggc ttg tcc agt ctc gaa gtc ttg aaa atg gct							1344
226	Asn Gly Ile Phe Asn Gly Leu Ser Ser Leu Glu Val Leu Lys Met Ala							
227		435		440		445		
229	ggc aat tct ttc cag gaa aac ttc ctt cca gat atc ttc aca gag ctg							1392
230	Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Glu Leu							
231		450		455		460		
233	aga aac ttg acc ttc ctg gac ctc tct cag tgt caa ctg gag cag ttg							1440
234	Arg Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu							
235	465		470		475		480	
237	tct cca aca gca ttt aac tca ctc tcc agt ctt cag gta cta aat atg							1488
238	Ser Pro Thr Ala Phe Asn Ser Leu Ser Ser Leu Gln Val Leu Asn Met							
239		485		490		495		
241	agc cac aac aac ttc ttt tca ttg gat acg ttt cct tat aag tgt ctg							1536
242	Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu							
243		500		505		510		
245	aac tcc ctc cag gtt ctt gat tac agt ctc aat cac ata atg act tcc							1584
246	Asn Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser							
247		515		520		525		
249	aaa aaa cag gaa cta cag cat ttt cca agt agt cta gct ttc tta aat							1632
250	Lys Lys Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn							
251		530		535		540		
253	ctt act cag aat gac ttt gct tgt act tgt gaa cac caa agt ttc ctg							1680
254	Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu							
255	545		550		555		560	
257	caa tgg atc aag gac cag agg cag ctc ttg gtg gaa gtt gaa cga atg							1728
258	Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Val Glu Arg Met							
259		565		570		575		
261	gaa tgt gca aca cct tca gat aag cag ggc atg cct gtg ctg agt ttg							1776
262	Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu							
263		580		585		590		
265	aat atc acc tgt cag atg aat aag acc atc att ggt gtg tcg gtc ctc							1824
266	Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Leu							
267		595		600		605		
269	agt gtg ctt gta gta tct gtt gta gca gtt ctg gtc tat aag ttc tat							1872
270	Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr							
271		610		615		620		
273	ttt cac ctg atg ctt ctt gct ggc tgc ata aag tat ggt aga ggt gaa							1920
274	Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu							
275	625		630		635		640	
277	aac atc tat gat gcc ttt gtt atc tac tca agc cag gat gag gac tgg							1968
278	Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp							
279		645		650		655		
281	gta agg aat gag cta gta aag aat tta gaa gaa ggg gtg cct cca ttt							2016
282	Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe							
283		660		665		670		

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286 Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala
287          675          680          685
289 gcc aac atc atc cat gaa ggt ttc cat aaa agc cga aag gtg att gtt      2112
290 Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val
291          690          695          700
293 gtg gtg tcc cag cac ttc atc cag agc cgc tgg tgt atc ttt gaa tat      2160
294 Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr
295 705          710          715          720
297 gag att gct cag acc tgg cag ttt ctg agc agt cgt gct ggt atc atc      2208
298 Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile
299          725          730          735
301 ttc att gtc ctg cag aag gtg gag aag acc ctg ctc agg cgg cag gtg      2256
302 Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Arg Gln Val
303          740          745          750
305 gag ctg tac cgc ctt ctc agc agg aac act tac ctg gag tgg gag gac      2304
306 Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp
307          755          760          765
309 agt gtc ctg ggg cgg cac atc ttc tgg aga cga ctc aga aaa gcc ctg      2352
310 Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu
311          770          775          780
313 ctg gat ggt aaa tca tgg aat cca gaa gga aca gtg ggt aca gga tgc      2400
314 Leu Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys
315 785          790          795          800
317 aat tgg cag gaa gca aca tct atc tga      2427
318 Asn Trp Gln Glu Ala Thr Ser Ile
319          805
322 <210> SEQ ID NO: 3
323 <211> LENGTH: 808
324 <212> TYPE: PRT
325 <213> ORGANISM: Pan troglodytes
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333 Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe
334          20          25          30
337 Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu
338          35          40          45
341 Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp
342          50          55          60
345 Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly
346 65          70          75          80
349 Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser
350          85          90          95
353 Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn
354          100          105          110
357 Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His
358          115          120          125
361 Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/532,153

DATE: 04/28/2005
TIME: 16:26:59

Input Set : A:\Seq Listing.ST25.txt
Output Set: N:\CRF4\04272005\J532153.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 198,683
Seq#:9; Xaa Pos. 198,683
Seq#:11; Xaa Pos. 635
Seq#:12; Xaa Pos. 635
Seq#:17; Xaa Pos. 14,462
Seq#:18; Xaa Pos. 14,462
Seq#:23; Xaa Pos. 758
Seq#:24; Xaa Pos. 758

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1198 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:8
L:1198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:624
M:341 Repeated in SeqNo=8
L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:192
M:341 Repeated in SeqNo=9
L:1830 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:11
L:1830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1920
L:2042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:624
L:2665 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:17
L:2665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:48
M:341 Repeated in SeqNo=17
L:2886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
M:341 Repeated in SeqNo=18
L:3885 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:23
L:3885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:2304
L:4101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:752